1632
6

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/416,267*

INPUT SET: S34718.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

```
1
2
3    (1)    General Information:
4
5        (i) APPLICANT: LI, YI
6                      SU, KUI
7                      LI, HAODONG
8
9       (ii) TITLE OF INVENTION: HUMAN CYTOKINE POLYPEPTIDE
10
11      (iii) NUMBER OF SEQUENCES: 9
12
13      (iv) CORRESPONDENCE ADDRESS:
14            (A) ADDRESSEE: Human Genome Sciences, Inc.
15            (B) STREET: 9410 Key West Avenue
16            (C) CITY: Rockville
17            (D) STATE: MD
18            (E) COUNTRY: USA
19            (F) ZIP: 20850
20
21       (v) COMPUTER READABLE FORM:
22            (A) MEDIUM TYPE: Floppy disk
23            (B) COMPUTER: IBM PC compatible
24            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27      (vi) CURRENT APPLICATION DATA:
28            (A) APPLICATION NUMBER: 09/416,267
29            (B) FILING DATE: OCT-12-1999
30            (C) CLASSIFICATION:
31
32    (viii) ATTORNEY/AGENT INFORMATION:
33            (A) NAME: Joseph J. Kenny
34            (B) REGISTRATION NUMBER: 43,710
35            (C) REFERENCE/DOCKET NUMBER: PF270P1
36
37      (ix) TELECOMMUNICATION INFORMATION:
38            (A) TELEPHONE: 301-309-8504
39            (B) TELEFAX: 301-309-8439
40
41
42    (2) INFORMATION FOR SEQ ID NO:1:
43
44        (i) SEQUENCE CHARACTERISTICS:
45            (A) LENGTH: 780 base pairs
46            (B) TYPE: nucleic acid
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47              (C) STRANDEDNESS: single
48              (D) TOPOLOGY: linear
49
50       (ii) MOLECULE TYPE: DNA (genomic)
51
52
53       (ix) FEATURE:
54              (A) NAME/KEY: sig_peptide
55              (B) LOCATION: 72..131
56
57       (ix) FEATURE:
58              (A) NAME/KEY: mat_peptide
59              (B) LOCATION: 132..740
60
61       (ix) FEATURE:
62              (A) NAME/KEY: CDS
63              (B) LOCATION: 72..740
64
65
66       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
67
68
69   GCACGAGGGC GACTTCGCGG GACCGTGGCG CATGTTTCCT GGGAGTTACT GATCATCTTC        60
70
71   TTTGAAGAAA C ATG AAG TTA CAC TAT GTT GCT GTG CTT ACT CTA GCC ATC        110
72              Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile
73              -20              -15              -10
74
75   CTG ATG TTC CTG ACA TGG CTT CCA GAA TCA CTG AGC TGT AAC AAA GCA        158
76   Leu Met Phe Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala
77        -5              1              5
78
79   CTC TGT GCT AGT GAT GTG AGC AAA TGC CTC ATT CAG GAG CTC TGC CAG        206
80   Leu Cys Ala Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln
81    10              15              20              25
82
83   TGC CGG CCG GGA GAA GGC AAT TGC TCC TGC TGT AAG GAG TGC ATG CTG        254
84   Cys Arg Pro Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu
85              30              35              40
86
87   TGT CTT GGG GCC CTT TGG GAC GAG TGC TGT GAC TGT GTT GGT ATG TGT        302
88   Cys Leu Gly Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys
89              45              50              55
90
91   AAT CCT CGA AAT TAT AGT GAC ACA CCT CCA ACT TCA AAG AGC ACA GTG        350
92   Asn Pro Arg Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val
93              60              65              70
94
95   GAG GAG CTG CAT GAA CCG ATC CCT TCT CTC TTC CGG GCA CTC ACA GAA        398
96   Glu Glu Leu His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu
97        75              80              85
98
99    GGA GAT ACT CAG TTG AAT TGG AAC ATC GTT TCT TTC CCT GTT GCA GAA       446
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100      Gly Asp Thr Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu
101       90                  95                 100                 105
102                                                                           494
103      GAA CTT TCA CAT CAT GAG AAT CTG GTT TCA TTT TTA GAA ACT GTG AAC
104      Glu Leu Ser His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn
105                          110                 115                 120
106                                                                           542
107      CAG CCA CAC CAC CAG AAT GTG TCT GTC CCC AGC AAT AAT GTT CAC GCG
108      Gln Pro His His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala
109                  125                 130                 135
110                                                                           590
111      CCT TAT TCC AGT GAC AAA GAA CAC ATG TGT ACT GTG GTT TAT TTT GAT
112      Pro Tyr Ser Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp
113              140                 145                 150
114                                                                           638
115      GAC TGC ATG TCC ATA CAT CAG TGT AAA ATA TCC TGT GAG TCC ATG GGA
116      Asp Cys Met Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly
117          155                 160                 165
118                                                                           686
119      GCA TCC AAA TAT CGC TGG TTT CAT AAT GCC TGC TGC GAG TGC ATT GGT
120      Ala Ser Lys Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly
121      170                 175                 180                 185
122                                                                           734
123      CCA GAA TGT ATT GAC TAT GGT AGT AAA ACT GTC AAA TGT ATG AAC TGC
124      Pro Glu Cys Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys
125                          190                 195                 200
126                                                                           780
127      ATG TTT TAAAGAAGAC AAATGCAAAC CAAAGCAACT TAGTAAAATA
128      Met Phe
129
130
131
132      (2) INFORMATION FOR SEQ ID NO:2:
133
134              (i) SEQUENCE CHARACTERISTICS:
135                      (A) LENGTH: 223 amino acids
136                      (B) TYPE: amino acid
137                      (D) TOPOLOGY: linear
138
139              (ii) MOLECULE TYPE: protein
140
141              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
142
143      Met Lys Leu His Tyr Val Ala Val Leu Thr Leu Ala Ile Leu Met Phe
144      -20                 -15                 -10                  -5
145
146      Leu Thr Trp Leu Pro Glu Ser Leu Ser Cys Asn Lys Ala Leu Cys Ala
147                       1                   5                  10
148
149      Ser Asp Val Ser Lys Cys Leu Ile Gln Glu Leu Cys Gln Cys Arg Pro
150                  15                  20                  25
151
152      Gly Glu Gly Asn Cys Ser Cys Cys Lys Glu Cys Met Leu Cys Leu Gly
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153                          30                    35                           40
154
155     Ala Leu Trp Asp Glu Cys Cys Asp Cys Val Gly Met Cys Asn Pro Arg
156        45                          50                    55                    60
157
158     Asn Tyr Ser Asp Thr Pro Pro Thr Ser Lys Ser Thr Val Glu Glu Leu
159                          65                                  70                    75
160
161     His Glu Pro Ile Pro Ser Leu Phe Arg Ala Leu Thr Glu Gly Asp Thr
162                          80                          85                    90
163
164     Gln Leu Asn Trp Asn Ile Val Ser Phe Pro Val Ala Glu Glu Leu Ser
165                  95                          100                   105
166
167     His His Glu Asn Leu Val Ser Phe Leu Glu Thr Val Asn Gln Pro His
168        110                         115                   120
169
170     His Gln Asn Val Ser Val Pro Ser Asn Asn Val His Ala Pro Tyr Ser
171     125                         130                   135                   140
172
173     Ser Asp Lys Glu His Met Cys Thr Val Val Tyr Phe Asp Asp Cys Met
174                         145                   150                         155
175
176     Ser Ile His Gln Cys Lys Ile Ser Cys Glu Ser Met Gly Ala Ser Lys
177                         160                   165                   170
178
179     Tyr Arg Trp Phe His Asn Ala Cys Cys Glu Cys Ile Gly Pro Glu Cys
180                  175                         180                   185
181
182     Ile Asp Tyr Gly Ser Lys Thr Val Lys Cys Met Asn Cys Met Phe
183        190                         195                   200
```

184
185   (2) INFORMATION FOR SEQ ID NO:3:
186
187   (i) SEQUENCE CHARACTERISTICS:
188   (A) LENGTH: 32 base pairs
189   (B) TYPE: nucleic acid
190   (C) STRANDEDNESS: single
191   (D) TOPOLOGY: linear
192
193   (ii) MOLECULE TYPE: other nucleic acid
194
195
196
197
198   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
199   32
200   GTACGGATCC AGCTGTAACA AAGCACTCTG TG
201
202   (2) INFORMATION FOR SEQ ID NO:4:
203
204   (i) SEQUENCE CHARACTERISTICS:
205   (A) LENGTH: 36 base pairs

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206          (B) TYPE: nucleic acid
207          (C) STRANDEDNESS: single
208          (D) TOPOLOGY: linear
209
210     (ii) MOLECULE TYPE: other nucleic acid
211
212
213
214
215     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:                       36
216
217   GTCAAGCTTT TAAAACATGC AGTTCATACA TTTGAC
218
219   (2) INFORMATION FOR SEQ ID NO:5:
220
221       (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 40 base pairs
223          (B) TYPE: nucleic acid
224          (C) STRANDEDNESS: single
225          (D) TOPOLOGY: linear
226
227     (ii) MOLECULE TYPE: other nucleic acid
228
229
230
231
232     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:                       40
233
234   GATAGGATCC GCCATCATGA AGTTACACTA TGTTGCTGTG
235
236   (2) INFORMATION FOR SEQ ID NO:6:
237
238       (i) SEQUENCE CHARACTERISTICS:
239          (A) LENGTH: 37 base pairs
240          (B) TYPE: nucleic acid
241          (C) STRANDEDNESS: single
242          (D) TOPOLOGY: linear
243
244     (ii) MOLECULE TYPE: other nucleic acid
245
246
247
248
249     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:                       37
250
251   GTCAGGTACC TTAAAACATG CAGTTCATAC ATTTGAC
252
253   (2) INFORMATION FOR SEQ ID NO:7:
254
255       (i) SEQUENCE CHARACTERISTICS:
256          (A) LENGTH: 67 base pairs
257          (B) TYPE: nucleic acid
258          (C) STRANDEDNESS: single
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SEQUENCE VERIFICATION REPORT
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